What is claimed is:

1. A method for constructing a strain of diploid fungal cells in which both alleles of a gene are modified, the method comprising the steps of:

(a) modifying a first allele of a gene in diploid fungal cells by recombination using a gene disruption cassette comprising a first nucleotide sequence encoding an expressible selectable marker, thereby providing heterozygous diploid fungal cells in which the first allele of the gene is inactivated; and

(b) modifying the second allele of the gene in the heterozygous diploid fungal cells by recombination using a promoter replacement fragment comprising a second nucleotide sequence encoding a heterologous promoter, such that expression of the second allele of the gene is regulated by the heterologous promoter; and

wherein the gene encodes a polypeptide consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NO.: 7001 to 7932.

2. A method of assembling a collection of diploid fungal cells each of which comprises modified alleles of a different gene, the method comprising the steps of:

(a) modifying a first allele of a first gene in diploid fungal cells by recombination using a gene disruption cassette comprising a first nucleotide sequence encoding an expressible selectable marker, thereby providing heterozygous diploid fungal cells in which the first allele of the gene is inactivated;

(b) modifying a second allele of the first gene in the heterozygous diploid fungal cells by recombination using a promoter replacement fragment comprising a second nucleotide sequence encoding a heterologous promoter, such that expression of the second allele of the gene is regulated by the heterologous promoter, thereby providing a first strain of diploid fungal cells comprising a modified allelic pair of the first gene; and

(c) repeating steps (a) and (b) a plurality of times, wherein a different gene is modified with each repetition, thereby providing the collection of diploid fungal cells each comprising the modified alleles of a different gene, and

wherein each different gene encodes a different polypeptide consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NO.: 7001 to 7932.

3. The method of claim 1 or 2, wherein the selectable marker in the gene disruption cassette is disposed between a first region and a second region, wherein the first region and the second region hybridize separately to non-contiguous regions of the first

allele of the gene in the diploid fungal cells.

4. The method of claim 3, wherein the selectable marker is selected from the group consisting of CaSAT1, CaBSR1, CaURA3, CaHIS3, CaLEU2, CaTRP1, and combinations thereof.

5. The method of claim 1, wherein the diploid fungal cells are cells of fungal species selected from the group consisting of *Aspergillus fumigatus*, *Aspergillus niger*, *Aspergillus flavis*, *Candida albicans*, *Candida tropicalis*, *Candida parapsilopsis*, *Candida krusei*, *Cryptococcus neoformans*, *Coccidioides immitis*, *Exophalia dermatiditis*, *Fusarium oxysporum*, *Histoplasma capsulatum*, *Pneumocystis carinii*, *Trichosporon beigelii*, *Rhizopus arrhizus*, *Mucor rouxii*, *Rhizomucor pusillus*, *Absidia corymbigera*, *Botrytis cinerea*, *Erysiphe graminis*, *Magnaporthe grisea*, *Puccinia recodita*, *Septoria triticii*, *Tilletia controversa*, and *Ustilago maydis*.

6. The method of claim 1 or 2, wherein the gene corrresponds to an open reading frame selected from the group consisting of SEQ ID NO: 6001-6932.

7. The method of claim 1 or 2, wherein the method further comprises (c) introducing a nucleotide sequence encoding a transactivation fusion protein that is expressible in the diploid fungal cell, said transactivation fusion protein comprising a DNA binding domain and a transcription activation domain; and wherein the heterologous promoter in the promoter replacement fragment comprises at least one copy of a nucleotide sequence which is bound by the DNA binding domain of the transactivation fusion protein, such that binding of the transactivation fusion protein increases transcription from the heterologous promoter.

8. The method of claim 7, wherein the promoter replacement fragment further comprises a selectable marker.

9. The method of claim 8, wherein the selectable marker is selected from the group consisting of CaHIS3, CaSAT1, CaBSR1, CaURA3, CaLEU2, CaTRP1, and combinations thereof.

10. A strain of diploid fungal cells comprising modified alleles of a gene, wherein the first allele of the gene is inactivated by a gene disruption cassette comprising a nucleotide sequence encoding an expressible selectable marker; and the expression of the

second allele of the gene is regulated by a heterologous promoter that is operably linked to the coding region of the second allele of the gene, and wherein the gene encodes a polypeptide consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NO.: 7001 to 7932.

11. The diploid fungal cells of claim 10 further comprising a nucleotide sequence encoding a transactivation fusion protein that is expressible in the diploid fungal cell, said transactivation fusion protein comprising a DNA binding domain and a transcription activation domain; and wherein the heterologous promoter in the promoter replacement fragment comprises at least one copy of a nucleotide sequence which is bound by the DNA binding domain of the transactivation fusion protein, such that binding of the transactivation fusion protein modulates transcription from the heterologous promoter.

12. The strain of diploid fungal cells of claim 10 or 11, wherein the gene is a gene essential for the growth and/or survival of the cells; or contributes to the virulence and/or pathogenicity of the fungal cells against a host organism..

13. The strain of diploid fungal cells of claim 10 or 11, wherein the gene corrresponds to an open reading frame selected from the group consisting of SEQ ID NO: 6001-6932.

14. A collection of diploid fungal strains comprising diploid strains of claim 10, wherein substantially all the different genes that encode the amino acid sequences of SEQ ID NO: 7001 to 7932 are modified and are present in different diploid strains in the collection.

15. A collection of diploid fungal strains of claim 10 each comprising the modified alleles of a different gene, wherein each gene is essential for the growth and/or survival of the cells, and wherein each gene encodes a polypeptide consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NO: 7001 to 7932.

16. The collection of diploid fungal strains of claim 15, wherein each of the genes corrresponds to an open reading frame selected from the group consisting of SEQ ID NO: 6001-6932.

17. A collection of diploid fungal strains of claim 10 each strain comprising the modified alleles of a different gene, wherein each gene contributes to the

virulence and/or pathogenicity of the cells to a host organism.

18. The collection of diploid fungal strains of claim 17, wherein substantially all of the genes in the genome of the diploid fungus that contribute to the virulence and/or pathogenicity of the fungal cells against a host organism are modified and present in the collection.

19. The collection of diploid fungal strains of claim 14, wherein the essential genes present in the collection all share a characteristic selected from the group consisting of: similar biological activity, similar intracellular localization, structural homology, sequence homology, cidal terminal phenotype, static terminal phenotype, sequence homology to human genes, and exclusivity with respect to the organism.

20. The collection of diploid fungal strains of claim 14, 15, 17, or 19 wherein the cells of each strain further comprise at least one molecular tag of about 20 nucleotides, the sequence of which is unique to each strain.

21. The collection of claim 20, wherein the molecular tag is disposed within the gene disruption cassette.

22. A nucleic acid molecule microarray comprising a plurality of nucleic acid molecules, wherein each nucleic acid molecule comprises a nucleotide sequence that is hybridizable to a target nucleotide sequence selected from the group consisting of SEQ ID NO:6001 through to SEQ ID NO:6932.

23. A nucleic acid molecule microarray comprising a plurality of nucleic acid molecules, wherein each nucleic acid molecule comprises a nucleotide sequence that is hybridizable to the nucleotide sequence of a gene that is either essential to the growth of a diploid fungal cell or contributes to the virulence and/or pathogenicity of the diploid fungal cells against a host organism, and wherein each of the gene encodes a polypeptide consisting essentially of an amino acid sequence selected from the group consisting of SEQ ID NO.: 7001 to 7932.

24. A method for identifying a gene that is essential to the survival of a fungus comprising the steps of:

(a) culturing the diploid fungal cells of claim 10 under conditions wherein the second allele of the gene is substantially underexpressed or not expressed; and

(b) determining viability of the cells; whereby a loss or reduction of viability as compared to a control indicates that the modified gene is essential to the survival of the fungus.

25. A method for identifying a gene that is essential to the growth of a fungus comprising the steps of:

(a) culturing the diploid fungal cells of claim 10 under conditions wherein the second allele of the gene is substantially underexpressed or not expressed; and

(b) determining growth of the cells; whereby a loss or reduction of growth of the cells as compared to a control indicates that the modified gene is essential to the growth of the fungus.

26. A method for identifying a gene that contributes to the virulence and/or pathogenicity of a fungus comprising the steps of:

(a) culturing diploid fungal cells of claim 10 or 11 under conditions wherein the second allele of the gene is substantially underexpressed or not expressed; and

(b) determining the virulence and/or pathogenicity of the cells toward a host cell or organism; whereby a reduction of virulence and/or pathogenicity as compared to a control indicates that the modified gene contributes to the virulence and/or pathogenicity of the fungus.

27. A method for identifying a gene that contributes to the resistance of a diploid fungus to an antifungal agent comprising the steps of:

(a) culturing the diploid fungal cells of claim 10 under conditions wherein the second allele is substantially overexpressed and in the presence of the antifungal agent; and

(b) determining the viability of the cells; whereby an increase in viability as compared to a control indicates that the modified gene contributes to the resistance of the diploid fungus to the antifungal agent.

28. A method for identifying an antifungal agent that inhibits the growth of a diploid fungus comprising the steps of:

(a) providing diploid fungal cells of claim 12; and

(b) culturing the diploid fungal cells under conditions wherein the second allele of the gene is underexpressed and in the presence of a test compound; whereby a loss or reduction of growth of the diploid fungal cells as compared to a control

indicates that the test compound is an antifungal agent.

29. A method for identifying a therapeutic agent for treatment of a mammalian disease, the method comprising the steps of:

(a) providing diploid cells of claim 10, wherein the modified gene in the diploid cells is an essential gene and displays sequence homology to a mammalian gene associated with the disease;

(b) culturing diploid fungal cells under conditions wherein the second allele of the gene is overexpressed or underexpressed and in the presence of a test compound;

whereby a difference in growth of the diploid fungal cells as compared to a control indicates that the test compound is a therapeutic agent.

30. A method for correlating changes in the levels of proteins with the inhibition of growth or proliferation of a diploid fungal cell, the method comprising the steps of:

(a) generating a first protein expression profile for a control diploid fungal cell which comprises two wild type alleles of the gene;

(b) culturing diploid fungal cells of claim 12 under conditions wherein the second allele of the gene is substantially underexpressed, not expressed or overexpressed, and generating a second protein expression profile for the cultured cells; and

(c) comparing the first protein expression profile with the second protein expression profile to identify changes in the levels of proteins.

31. A method for correlating changes in the levels of gene transcripts with the inhibition of growth or proliferation of a diploid fungal cell, the method comprising the steps of:

(a) generating a transcription profile for a control diploid fungal cell which comprises two wild type alleles of the gene;

(b) culturing diploid fungal cells of claim 12 under conditions wherein the second allele of the gene is substantially underexpressed, not expressed or overexpressed and generating a second transcription profile for the cultured cells; and

(c) comparing the first transcription profile with the second transcription profile to identify changes in the levels of gene transcripts.

32. A purified or isolated nucleic acid molecule comprises a nucleotide

sequence encoding a gene product required for proliferation of *Candida albicans*, wherein said gene product consisting essentially of an amino acid sequence of one of SEQ ID NO: 7001 to 7932.

33. The nucleic acid molecule of claim 32, wherein said nucleotide sequence is one of SEQ ID NO:6001 to 6932.

34. A nucleic acid molecule comprising a fragment of one of SEQ ID NO.:6001 to 6932, said fragment selected from the group consisting of fragments comprising at least 10, at least 20, at least 25, at least 30, at least 50 and at least 100 consecutive nucleotides of one of SEQ ID NO: 6001 to 6932.

35. A nucleic acid molecule comprising a nucleotide sequence that hybridizes under stringent condition to a second nucleic acid molecule consisting of (a) a nucleotide sequence selected from the group consisting of one of SEQ ID NO.: 6001 to 6932, or (b) a nucleotide sequence that encodes a polypeptide consisting of an amino acid sequence selected from the group consisting of one of SEQ ID NO.: 7001 to 7932; wherein said stringent condition comprises hybridization to filter-bound DNA in 6x sodium chloride/sodium citrate (SSC) at about 45°C followed by one or more washes in 0.2xSSC/0.1% SDS at about 50-65°C.

36. The nucleic acid molecule of claim 34 or 35, which consists of the nucleotide sequence selected from the group consisting of one of SEQ ID NO.: 4001 to 4932, and 5001 to 5932.

37. A purified or isolated nucleic acid molecule obtained from an organism other than *Candida albicans* or *Saccharomyces cerevisiae* comprising a nucleotide sequence having at least 30% identity to a sequence selected from the group consisting of SEQ ID NO: 6001-6932, fragments comprising at least 25 consecutive nucleotides of SEQ ID NO:6001-6932, the sequences complementary to SEQ ID NO:6001-6932 and the sequences complementary to fragments comprising at least 25 consecutive nucleotides of SEQ ID NO:6001-6932, as determined using BLASTN version 2.0 with the default parameters.

38. The purified or isolated nucleic acid molecule of Claim 37, wherein said organism is selected from the group consisting of *Absidia corymbigera, Aspergillus flavis, Aspergillus fumigatus, Aspergillus niger, Botrytis cinerea, Candida albicans,*

Candida dublinensis, Candida glabrata, Candida krusei, Candida parapsilopsis, Candida tropicalis, Coccidioides immitis, Cryptococcus neoformans, Erysiphe graminis, Exophalia dermatiditis, Fusarium oxysporum, Histoplasma capsulatum, Magnaporthe grisea, Mucor rouxii, Pneumocystis carinii, Puccinia graminis, Puccinia recodita, Puccinia striiformis, Rhizomucor pusillus, Rhizopus arrhizus, Septoria avenae, Septoria nodorum, Septoria triticii, Tilletia controversa, Tilletia tritici, Trichosporon beigelii, and Ustilago maydis.

39. A vector comprising a promoter operably linked to the nucleic acid molecule of claim 32, 33, 34, 35, or 37.

40. The vector of Claim 39, wherein said promoter is regulatable.

41. The vector of Claim 39, wherein said promoter is active in an organism selected from the group consisting of *Absidia corymbigera, Aspergillus flavis, Aspergillus fumigatus, Aspergillus niger, Botrytis cinerea, Candida albicans, Candida dublinensis, Candida glabrata, Candida krusei, Candida parapsilopsis, Candida tropicalis, Coccidioides immitis, Cryptococcus neoformans, Erysiphe graminis, Exophalia dermatiditis, Fusarium oxysporum, Histoplasma capsulatum, Magnaporthe grisea, Mucor rouxii, Pneumocystis carinii, Puccinia graminis, Puccinia recodita, Puccinia striiformis, Rhizomucor pusillus, Rhizopus arrhizus, Septoria avenae, Septoria nodorum, Septoria triticii, Tilletia controversa, Tilletia tritici, Trichosporon beigelii, and Ustilago maydis.*

42. A host cell containing the vector of claim 39.

43. A purified or isolated polypeptide comprising an amino acid sequence selected from the group consisting of one of SEQ ID NO: 63 to 123.

44. A purified or isolated polypeptide obtained from an organism other than *Candida albicans* or *Saccharomyces cerevisiae* comprising an amino acid sequence having at least 30% similarity to an amino acid sequence selected from the group consisting of one of SEQ ID NO: 7001 to 7932 as determined using FASTA version 3.0t78 with the default parameters.

45. The polypeptide of Claim 44, wherein said organism is selected from the group consisting of *Absidia corymbigera, Aspergillus flavis, Aspergillus fumigatus, Aspergillus niger, Botrytis cinerea, Candida albicans, Candida dublinensis, Candida glabrata, Candida krusei, Candida parapsilopsis, Candida tropicalis, Coccidioides immitis,*

Cryptococcus neoformans, Erysiphe graminis, Exophalia dermatiditis, Fusarium oxysporum, Histoplasma capsulatum, Magnaporthe grisea, Mucor rouxii, Pneumocystis carinii, Puccinia graminis, Puccinia recodita, Puccinia striiformis, Rhizomucor pusillus, Rhizopus arrhizus, Septoria avenae, Septoria nodorum, Septoria triticii, Tilletia controversa, Tilletia tritici, Trichosporon beigelii, and Ustilago maydis.

46. A fusion protein comprising a fragment of a first polypeptide fused to a second polypeptide, said fragment consisting of at least 6 consecutive residues of an amino acid sequence selected from one of SEQ ID NO: 7001 to 7932.

47. A method of producing a polypeptide, said method comprises introducing into a cell, a vector comprising a promoter operably linked to a nucleotide sequence encoding a polypeptide consisting of an amino acid sequence selected from the group consisting of one of SEQ ID NO: 7001 to 7932; and culturing the cell such that the nucleotide sequence is expressed.

48. A method of producing a polypeptide, said method comprising providing a cell which comprises a heterologous promoter operably linked to a nucleotide sequence encoding a polypeptide consisting of an amino acid sequence selected from the group consisting of one of SEQ ID NO: 7001 to 7932; and culturing the cell such that the nucleotide sequence is expressed.

49. A method for identifying a compound which modulates the activity of a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of one of SEQ ID NO:6001 to 6932, said method comprising:

(a) contacting said gene product with a compound; and

(b) determining whether said compound modulates the activity of said gene product.

50. The method of claim 49, wherein the activity of the gene product is inhibited.

51. The method of Claim 49, wherein said gene product is a polypeptide and said activity is selected from the group consisting of an enzymatic activity, carbon compound catabolism activity, a biosynthetic activity, a transporter activity, a transcriptional activity, a translational activity, a signal transduction activity, a DNA replication activity, and a cell division activity.

52. A method of eliciting an immune response in an animal, comprising introducing into the animal a composition comprising an isolated polypeptide, the amino acid sequence of which comprises at least 6 consecutive residues of one of SEQ ID NO: 7001 to 7932.

53. A strain of *Candida albicans* wherein a first allele of a gene comprising a nucleotide sequence selected from the group consisting of one of SEQ ID NO: 6001 to 6932 is inactive and a second allele of the gene is under the control of a heterologous promoter.

54. A strain of *Candida albicans* comprising a nucleic acid molecule comprising a nucleotide sequence selected from one of SEQ ID NO: 6001 to 6932 under the control of a heterologous promoter.

55. The strain of claim 53 or 54, wherein said heterologous promoter is regulatable.

56. A method of identifying a compound or binding partner that binds to a polypeptide comprising an amino acid sequence selected from the group consisting of one of SEQ ID NO: 7001 to 7932 or a fragment thereof said method comprising:

(a) contacting the polypeptide or fragment thereof with a plurality of compounds or a preparation comprising one or more binding partners; and

(b) identifying a compound or binding partner that binds to the polypeptide or fragment thereof.

57. A method for identifying a compound having the ability to inhibit growth or proliferation of *Candida albicans*, said method comprising the steps of:

(a) reducing the level or activity of a gene product encoded by a nucleic acid selected from the group consisting of SEQ ID NO:6001 to 6932 in a *Candida albicans* cell relative to a wild type cell, wherein said reduced level is not lethal to said cell;

(b) contacting said cell with a compound; and

(c) determining whether said compound inhibits the growth or proliferation of said cell.

58. The method of Claim 57, wherein said step of reducing the level or activity of said gene product comprises transcribing a nucleotide sequence encoding said

gene product from a regulatable promoter under conditions in which said gene product is expressed at said reduced level.

59. The method of claim 58, wherein said gene product is a polypeptide comprising a sequence selected from the group consisting of polypeptides encoded by SEQ ID NO: 7001 to 7932.

60. A method for inhibiting growth or proliferation of *Candida albicans* cells comprising contacting the cells with a compound that (i) reduce the level of or inhibit the activity of a nucleotide sequence selected from the group consisting of SEQ ID NO: 6001 to 6932, or (ii) reduce the level of or inhibit the activity of a gene product encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 6001 to 6932.

61. The method of claim 60, wherein said gene product is a polypeptide comprising an amino acid sequence selected from the group consisting of polypeptides encoded by SEQ ID NO: 7001 to 7932.

62. The method of claim 60, wherein the compound is an antibody, a fragment of an antibody, an antisense nucleic acid molecule, or a ribozyme.

63. A method for manufacturing an antimycotic compound comprising the steps of:

(a) screening a pluralities of candidate compounds to identify a compound that reduces the activity or level of a gene product encoded by a nucleotide sequence selected from the group consisting of SEQ ID NO: 6001 to 6932; and

(b) manufacturing the compound so identified.

64. The method of claim 63, wherein said gene product is a polypeptide comprising an amino acid sequence selected from the group consisting of polypeptides encoded by SEQ ID NO: 6001 to 6932.

65. A method for treating an infection of a subject by *Candida albicans* comprising administering a pharmaceutical composition comprising a therapeutically effective amount of a compound that reduces the activity or level of a gene product encoded by a nucleic acid comprising a sequence selected from the group consisting of SEQ ID NO: 6001 to 6932 and a pharmaceutically acceptable carrier, to said subject.

66. The method of claim 65, wherein the compound is an antibody, a fragment of an antibody, an antisense nucleic acid molecule, or a ribozyme.

67. A method for preventing or containing contamination of an object by *Candida albicans* comprising contacting the object with a composition comprising an effective amount of a compound that reduces the activity or level of a gene product encoded by a nucleic acid comprising a sequence selected from the group consisting of SEQ ID NO: 6001 to 6932.

68. A method for preventing or inhibiting formation on a surface of a biofilm comprising *Candida albicans*, said method comprising contacting the surface with a composition comprising an effective amount of a compound that reduces the activity or level of a gene product encoded by a nucleic acid comprising a sequence selected from the group consisting of SEQ ID NO: 6001 to 6932.

69. A pharmaceutical composition comprising a therapeutically effective amount of an agent which reduces the activity or level of a gene product encoded by a nucleic acid selected from the group consisting of SEQ ID NO: 6001 to 6932 in a pharmaceutically acceptable carrier.

70. The method of claim 65, wherein said subject is selected from the group consisting of a plant, a vertebrate, a mammal, an avian, and a human.

71. An antibody preparation which binds the polypeptide of claim 43 or 44.

72. The antibody preparation of claim 71 which comprises a monoclonal antibody.

73. A method for evaluating a compound against a target gene product encoded by a nucleotide sequence comprising one of SEQ ID NO: 6001 to 6932, said method comprising the steps of:

(a) contacting wild type diploid fungal cells with the compound and generating a first protein expression profile;

(b) determining the protein expression profile of diploid fungal cells of claim 12 which have been cultured under conditions wherein the second allele of the target gene is substantially underexpressed, not expressed or overexpressed and

generating a second protein expression profile for the cultured cells; and

(c) comparing the first protein expression profile with the second protein expression profile to identify similarities in the profiles.

74. A method for evaluating a compound against a target gene product encoded by a nucleotide sequence comprising one of SEQ ID NO: 6001 to 6932, said method comprising the steps of:

(a) contacting wild type diploid fungal cells with the compound and generating a first transcription profile;

(b) determining the transcription profile of diploid fungal cells of claim 12 which have been cultured under conditions wherein the second allele of the target gene is substantially underexpressed, not expressed or overexpressed and generating a second transcription profile for the cultured cells; and

(c) comparing the first transcription profile with the second transcription profile to identify similarities in the profiles.

75. A method for identifying an antimycotic compound comprising screening a plurality of compounds to identify a compound that reduces the activity or level of a gene product, said gene product being encoded by a nucleotide sequence that is naturally occurring in *Saccharomyces cerevisiae* and that is the ortholog of a gene having a nucleotide sequence selected from the group consisting of SEQ ID NO: 6001 to 6932.

76. A computer or a computer readable medium that comprises at least one nucleotide sequence selected from the group consisting of SEQ ID NO: 1-932, 1001-1932, 2001-2932, 3001-3932, 4001-4932, 5001-5932, and 6001-6932, or at least one amino acid sequence selected from the group consisting of SEQ ID NO: 7001-7932.

77. A method assisted by a computer for identifying a putatively essential gene of a fungus, comprising detecting sequence homology between a fungal nucleotide sequence or fungal amino acid sequence with at least one nucleotide sequence selected from the group consisting of SEQ ID NO: 6001-6932, or at least one amino acid sequence selected from the group consisting of SEQ ID NO: 7001-7932.